



#9

A-690.ST25.txt
SEQUENCE LISTING

<110> KOHNO, TADAHIKO

<120> APO-AI/AII PEPTIDE DERIVATIVES

<130> A-690

<140> 09/840,669

<141> 2001-04-23

<150> 60/198,920

<151> 2000-04-21

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 684

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(684)

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Met	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
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ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	96
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
			20					25					30			

atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	144
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
		35					40					45				

cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	192
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
	50					55					60					

gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	240
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	
65					70					75					80	

tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	288
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	
				85					90					95		

ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	336
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	
			100					105					110			

atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	384
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	
		115					120					125				

gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	432
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	
	130					135					140					

agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	480
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	

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145		150		155		160	
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct							528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro							
		165		170		175	
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc							576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr							
		180		185		190	
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg							624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val							
		195		200		205	
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg							672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu							
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tct ccg ggt aaa							684
Ser Pro Gly Lys							
225							

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Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser															
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His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu															
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Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr															
65				70				75					80		
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn															
			85				90						95		
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro															
			100				105						110		
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln															
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Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val															
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Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val															
145				150				155					160		

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 210 215 220

Ser Pro Gly Lys
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Gly Gly Gly Lys Gly Gly Gly Gly
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<210> 4
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 <212> PRT
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<210> 6
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Ala Phe

<210> 10
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 <212> PRT
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 <223> Preferred embodiments
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 <221> misc_feature
 <222> (18)..(18)
 <223> Attached by optional linker to identical sequence, which is attached by optional linker to an Fc domain

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Ala Phe

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 <222> (18)..(18)
 <223> Attached by optional linker to an identical sequence

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Asp	Trp	Leu	Lys	Ala	Phe	Tyr	Asp	Lys	Val	Ala	Glu	Lys	Leu	Lys	Glu
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Ala Phe



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